UNITED STATES PATENT AND TRADEMARK OFFICE

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
08/936,657	09/24/1997	FRITZ ECKSTEIN	228213	9976

20306 7590 06/08/2004	EXAMINER
MCDONNELL BOEHNEN HULBERT & BERGHOFF LLP	SCHULTZ, JAMES

300 S. WACKER DRIVE	ART UNIT	PAPER NUMBER
32ND FLOOR	1635	
CHICAGO, IL 60606		

DATE MAILED: 06/08/2004

Please find below and/or attached an Office communication concerning this application or proceeding.

APPLICATION NO./ CONTROL NO.	FILING DATE	FIRST NAMED INVENTOR / PATENT IN REEXAMINATION	ATTORNEY DOCKET NO.

EXAMINER

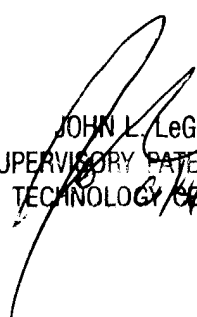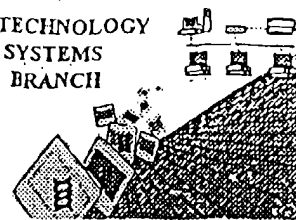| ART UNIT	PAPER

20040604

DATE MAILED:

Please find below and/or attached an Office communication concerning this application or proceeding.

Commissioner for Patents

Attached please find an error report generated while attempting to process the computer readable format (CRF) sequence listing submitted March 22, 2004. Sequences 12 and 13 define "N" as being of variable length, which is improper, since variable length entries are not permitted. Correction is required.

JOHN L. LeGUYADER
SUPERVISORY PATENT EXAMINER
TECHNOLOGY CENTER 1600

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information
Center (STIC) detected errors when processing the following computer readable
form:

Application Serial Number: _08/936,657A_

Source: _1FW/6_

Date Processed by STIC: _3/29/04_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE
   APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A
   NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221
Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
        http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is
a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the
United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission
   User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,
   2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office,
   Box Sequence, Room 4B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 08/936,657A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ___ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
  Wrapped Aminos was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
  prevent "wrapping."

2 ___ Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ___ Misaligned Amino The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
  Numbering use space characters, instead.

4 ___ Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
  ensure your subsequent submission is saved in ASCII text.

5 _/_ Variable Length Sequence(s) _12-13_ contain n's or Xaa's representing more than one residue. Per Sequence Rules,
  each n or Xaa can only represent a single residue. Please present the maximum number of each
  residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ___ PatentIn 2.0 A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
  "bug" sequences(s) _____ . Normally, PatentIn would automatically generate this section from the
  previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
  the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for
  Artificial or Unknown sequences.

7 ___ Skipped Sequences Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
  (OLD RULES) (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
  (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
  (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
  This sequence is intentionally skipped

  Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ___ Skipped Sequences Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
  (NEW RULES) <210> sequence id number
  <400> sequence id number
  000

9 ___ Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
  (NEW RULES) Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
  In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ___ Invalid <213> Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
  Response scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
  is Artificial Sequence

11 ___ Use of <220> Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
  Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
  "Unknown." Please explain source of genetic material in <220> to <223> section.
  (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 ___ PatentIn 2.0 Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
  "bug" resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
  listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ___ Misuse of n/Xaa "n" can only represent a single <u>nucleotide</u>; "Xaa" can only represent a single <u>amino acid</u>

IFW16

RAW SEQUENCE LISTING   DATE: 03/29/2004
PATENT APPLICATION: US/08/936,657A   TIME: 10:30:20

Input Set : A:\00-838-A.SequenceListing.txt
Output Set: N:\CRF4\03292004\H936657A.raw

```
 3 <110> APPLICANT: Sirna Therapeutics, Inc.
 5 <120> TITLE OF INVENTION: Modified Ribozymes
 7 <130> FILE REFERENCE: MBHB 00-838-A; 228/213
 9 <140> CURRENT APPLICATION NUMBER: US 08/936657A
10 <141> CURRENT FILING DATE: 1997-09-24
12 <150> PRIOR APPLICATION NUMBER: US 07/965,411
13 <151> PRIOR FILING DATE: 1993-08-09
15 <160> NUMBER OF SEQ ID NOS: 15
17 <170> SOFTWARE: PatentIn version 3.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 32
21 <212> TYPE: DNA
22 <213> ORGANISM: Artificial Sequence
24 <220> FEATURE:
25 <223> OTHER INFORMATION: Ribozyme
27 <400> SEQUENCE: 1
28 gatatcctga ctccctatag tgagtcgtat ta                        32
31 <210> SEQ ID NO: 2
32 <211> LENGTH: 36
33 <212> TYPE: DNA
34 <213> ORGANISM: Artificial Sequence
36 <220> FEATURE:
37 <223> OTHER INFORMATION: Ribozyme
39 <400> SEQUENCE: 2
40 taatacgact cactataggg agtcaggata tctgca                     36
43 <210> SEQ ID NO: 3
44 <211> LENGTH: 51
45 <212> TYPE: DNA
46 <213> ORGANISM: Artificial Sequence
48 <220> FEATURE:
49 <223> OTHER INFORMATION: Ribozyme
51 <400> SEQUENCE: 3
52 ggagtttcgg cctaacggcc tcatcagagg accctatagt gagtcgtatt a     51
55 <210> SEQ ID NO: 4
56 <211> LENGTH: 55
57 <212> TYPE: DNA
58 <213> ORGANISM: Artificial Sequence
60 <220> FEATURE:
61 <223> OTHER INFORMATION: Ribozyme
63 <400> SEQUENCE: 4
64 taatacgact cactataggg tcctctgatg aggccgttag gccgaaactc ctgca 55
67 <210> SEQ ID NO: 5
68 <211> LENGTH: 34
```

Does Not Comply
Corrected Diskette Needed

P.3

```
69 <212> TYPE: DNA
70 <213> ORGANISM: Artificial Sequence
72 <220> FEATURE:
73 <223> OTHER INFORMATION: Ribozyme
75 <400> SEQUENCE: 5
76 ggguccucug augaggccgu uaggccgaaa cucc                        34
79 <210> SEQ ID NO: 6
80 <211> LENGTH: 34
81 <212> TYPE: DNA
82 <213> ORGANISM: Artificial Sequence
84 <220> FEATURE:
85 <223> OTHER INFORMATION: Ribozyme
87 <220> FEATURE:
88 <221> NAME/KEY: misc_feature
89 <223> OTHER INFORMATION: All U nucleic acids are 2'-fluoro derivatives.
92 <400> SEQUENCE: 6
93 ggguccucug augaggccgu uaggccgaaa cucc                        34
96 <210> SEQ ID NO: 7
97 <211> LENGTH: 34
98 <212> TYPE: DNA
99 <213> ORGANISM: Artificial Sequence
101 <220> FEATURE:
102 <223> OTHER INFORMATION: Ribozyme
104 <220> FEATURE:
105 <221> NAME/KEY: misc_feature
106 <223> OTHER INFORMATION: All U nucleic acids are 2'-amino derivatives.
109 <400> SEQUENCE: 7
110 ggguccucug augaggccgu uaggccgaaa cucc                        34
113 <210> SEQ ID NO: 8
114 <211> LENGTH: 12
115 <212> TYPE: RNA
116 <213> ORGANISM: Artificial Sequence
118 <220> FEATURE:
119 <223> OTHER INFORMATION: Substrate
121 <400> SEQUENCE: 8
122 gggagucagg au                                               12
125 <210> SEQ ID NO: 9
126 <211> LENGTH: 12
127 <212> TYPE: RNA
128 <213> ORGANISM: Artificial Sequence
130 <220> FEATURE:
131 <223> OTHER INFORMATION: Substrate
133 <220> FEATURE:
134 <221> NAME/KEY: misc_feature
135 <223> OTHER INFORMATION: All U nucleotides are 2'-fluoro derivatives
138 <400> SEQUENCE: 9
139 gggagucagg au                                               12
142 <210> SEQ ID NO: 10
143 <211> LENGTH: 12
```

```
144 <212> TYPE: RNA
145 <213> ORGANISM: Artificial Sequence
147 <220> FEATURE:
148 <223> OTHER INFORMATION: Substrate
150 <220> FEATURE:
151 <221> NAME/KEY: misc_feature
152 <222> LOCATION: (7)..(7)
153 <223> OTHER INFORMATION: 2'-fluoro derivative
156 <400> SEQUENCE: 10
157 gggagucagg au                                              12
160 <210> SEQ ID NO: 11
161 <211> LENGTH: 12
162 <212> TYPE: RNA
163 <213> ORGANISM: Artificial Sequence
165 <220> FEATURE:
166 <223> OTHER INFORMATION: Substrate
168 <220> FEATURE:
169 <221> NAME/KEY: misc_feature
170 <222> LOCATION: (6)..(6)
171 <223> OTHER INFORMATION: 2'-amino derivative
174 <400> SEQUENCE: 11
175 gggagucagg au                                              12
178 <210> SEQ ID NO: 12
179 <211> LENGTH: 13
180 <212> TYPE: DNA
181 <213> ORGANISM: Artificial Sequence
183 <220> FEATURE:
184 <223> OTHER INFORMATION: Substrate
186 <220> FEATURE:
187 <221> NAME/KEY: misc_feature
188 <222> LOCATION: (13)..(13)
189 <223> OTHER INFORMATION: N stands for any one or more A, T, G, C.
192 <400> SEQUENCE: 12
```

W--> **193 gggagucagg aun**   13

```
196 <210> SEQ ID NO: 13
197 <211> LENGTH: 13
198 <212> TYPE: DNA
199 <213> ORGANISM: Artificial Sequence
201 <220> FEATURE:
202 <223> OTHER INFORMATION: Substrate
204 <220> FEATURE:
205 <221> NAME/KEY: misc_feature
206 <223> OTHER INFORMATION: All U nucleotides are 2'-fluoro derivatives.
209 <220> FEATURE:
210 <221> NAME/KEY: misc_feature
211 <222> LOCATION: (13)..(13)
212 <223> OTHER INFORMATION: N stands for one or more modified or unmodified nucleotides.
215 <400> SEQUENCE: 13
```

W--> **216 gggagucagg aun**   13

variable length is not permitted.
See item 5 on Error Summary Sheet.

same error

RAW SEQUENCE LISTING   DATE: 03/29/2004
PATENT APPLICATION: US/08/936,657A   TIME: 10:30:20

Input Set : A:\00-838-A.SequenceListing.txt
Output Set: N:\CRF4\03292004\H936657A.raw

```
219 <210> SEQ ID NO: 14
220 <211> LENGTH: 12
221 <212> TYPE: DNA
222 <213> ORGANISM: Artificial Sequence
224 <220> FEATURE:
225 <223> OTHER INFORMATION: Substrate
227 <220> FEATURE:
228 <221> NAME/KEY: misc_feature
229 <223> OTHER INFORMATION: All U nucleotides are 2'-fluoro derivatives.
232 <400> SEQUENCE: 14
233 gggagucagg au                                              12
236 <210> SEQ ID NO: 15
237 <211> LENGTH: 36
238 <212> TYPE: DNA
239 <213> ORGANISM: Artificial Sequence
241 <220> FEATURE:
242 <223> OTHER INFORMATION: Ribozyme
244 <400> SEQUENCE: 15
245 cacaacacug augaggccgu uaggccgaaa cgggca                    36
```

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 03/29/2004
PATENT APPLICATION: **US/08/936,657A**   TIME: 10:30:21

Input Set : **A:\00-838-A.SequenceListing.txt**
Output Set: **N:\CRF4\03292004\H936657A.raw**

<u>Please Note:</u>
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:12; N Pos. 13
Seq#:13; N Pos. 13

VERIFICATION SUMMARY
PATENT APPLICATION: **US/08/936,657A**

DATE: 03/29/2004
TIME: 10:30:21

Input Set : **A:\00-838-A.SequenceListing.txt**
Output Set: **N:\CRF4\03292004\H936657A.raw**

L:193 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0
L:216 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0

3/29/04